

Strategic Environmental Assessments Division's

BIOGEOGRAPHY PROGRAM:

**Habitat Suitability Index Modeling:
Species Habitat Suitability Index Values
Technical Guidelines**

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Habitat Suitability Index Modeling

Purpose

The purpose of this document is to provide a springboard for discussions on developing suitability index (SI) values for Habitat Suitability Modeling (HSI) modeling. It is intended to aid in the development of the Florida Estuarine Living Marine Resources Program (FLELMR) project between the Florida Marine Research Institute and NOAA's Strategic Environmental Assessments Division (Rubec et al., 1997). SI values are positively related to a species affinity along the gradient of each environmental variable incorporated in the model. HSI model results represent the interactions of those physical characteristics and how suitable each combination, or habitat, is to a given species (Christensen et al., 1997).

Literature Review as a Supplement to HSI Modeling

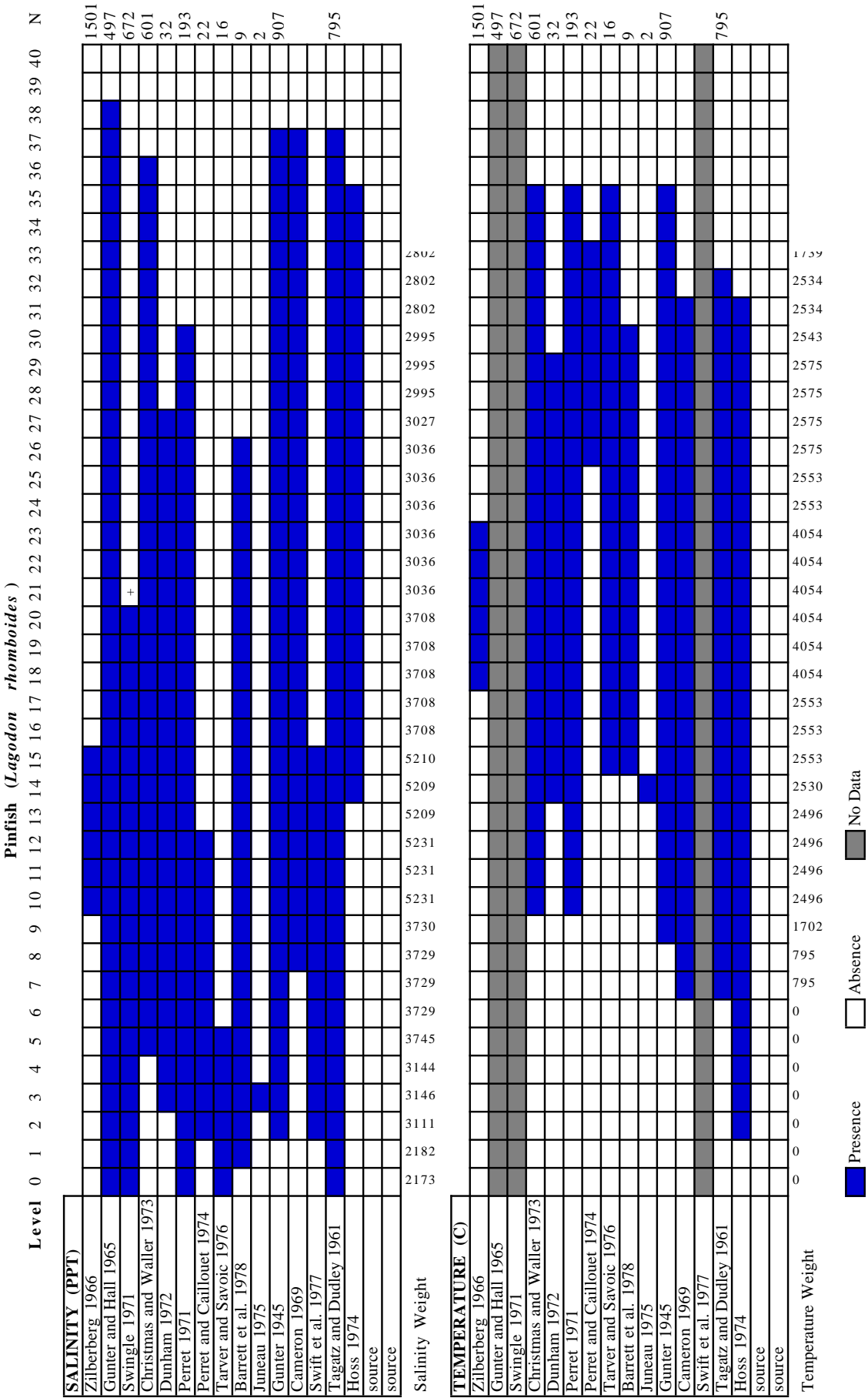
The first step in developing seascape HSI models is to initiate a comprehensive data and literature search. This is coupled with an expert review process to select an appropriate set of environmental and biological variables to model. A steering committee comprised of fisheries biologists, commercial fishermen, chemical oceanographers, hydrographers, and living resource managers is assembled to provide recommendations. A species occurrence matrix (presence/absence) is then developed for each environmental parameter selected in one unit increments — salinity (ppt), water temperature (°C), dissolved oxygen content (mg/l), depth (m), presence of submerged aquatic vegetation (i.e., *Halodule wrightii*), and presence of emergent wetland vegetation (i.e., *Spartina alterniflora*) — to generate SI values. These matrices enabled identification of critical values above and/or below which species were never present. Although interactions commonly occur between environmental variables, this model assumes their independence from one another. Individual SI's can be derived under the assumption that all other parameters are held constant at, or near, their species-specific optimum. Under these assumptions, complete absence indicated zero suitability, and SI coefficients are set accordingly.

The following represents an example of the literature review process currently in preliminary stages. This process is presented as a method for analyzing and familiarizing oneself with data available in the scientific literature. Relative abundances gathered from the literature can be used in HSI modeling with some degree of reliability in the absence of quantitative data, but is most useful as a supplement to fill gaps in quantitative datasets.

Pinfish are used as an example here and a presence/absence matrix has been developed from the literature for salinity and temperature (Table 1). It is important to note that discussion of relative abundance in the literature has not yet been taken into account. Only overall totals have been considered to this point. Additional analysis would include commentary on relative abundance.

Relative abundances across environmental increments are weighted by number of observa

Table 1. Presence-absence matrix based upon literature review of pinfish research. N is the sample size observed in each source. Weight represents sum of sample sizes at a given salinity or temperature level.



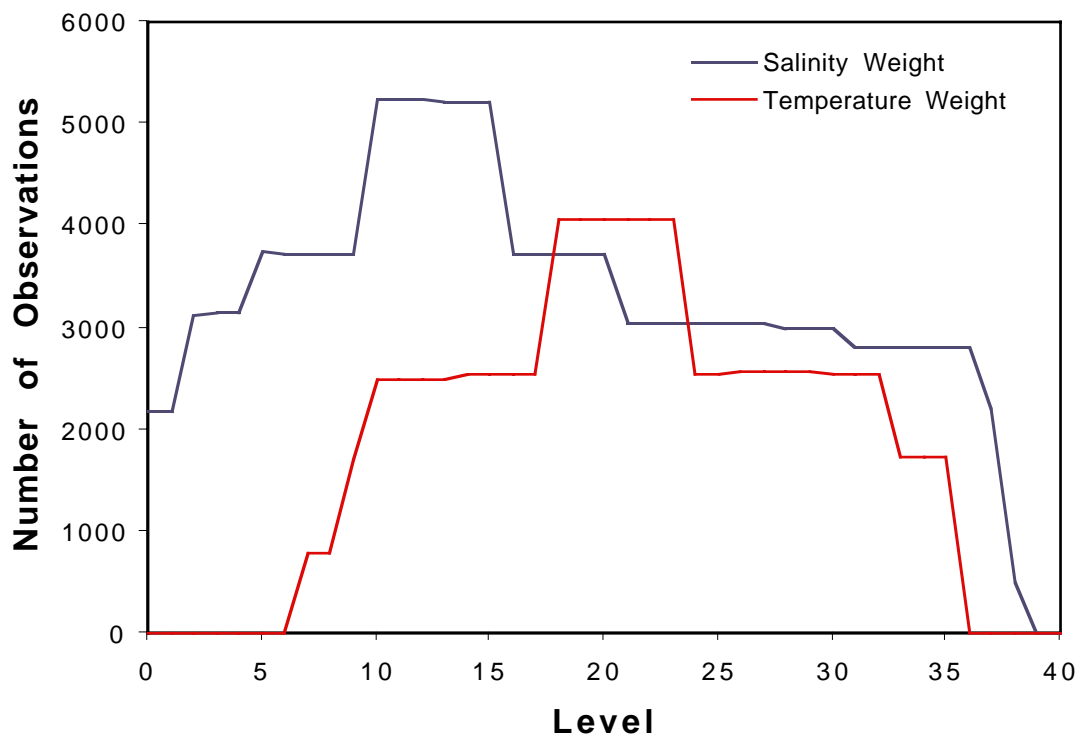


Figure 1. Relative occurrence of pinfish in the scientific literature by salinity and temperature increments. Each level is weighted with the number of observations at that level.

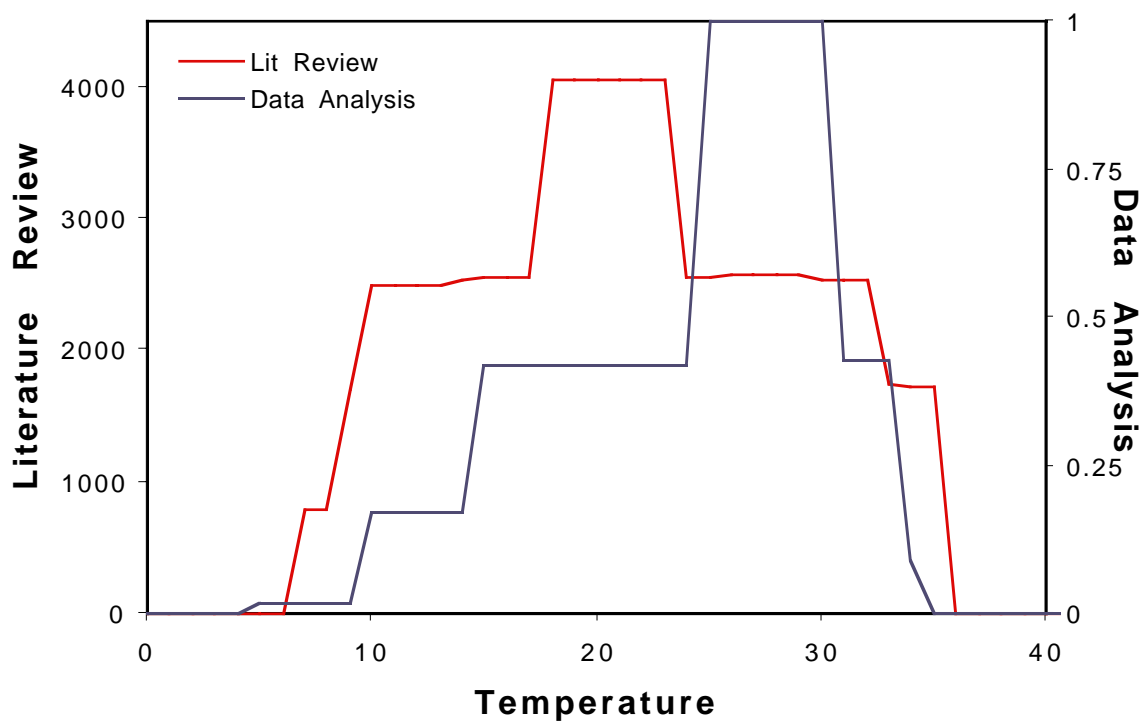
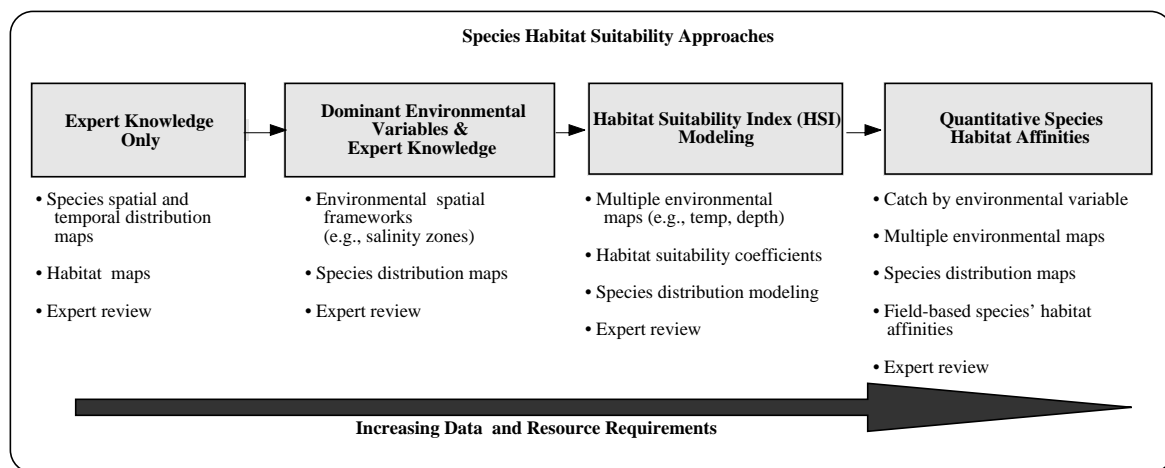


Figure 2. Comparison of relative occurrence derived from literature and preliminary abundance calculated by cumulative distribution analysis of fisheries independent monitoring by Texas Parks and Wildlife Department.

tions at each level in sources reporting pinfish at that level (Figure 1). Comparison of these data with those derived from a cumulative distribution analysis are presented in figure 2. Relative abundances are not necessarily the same at each level, but range of occurrence is similar.

Recently BCB has developed a continuum of approaches to evaluate the efficacy of SI derivation (Figure 3). This continuum is best represented by the composite of points along a progression of data type, requirement, availability, reliability, and robustness. The range of approaches include reliance upon “qualitative” literature review to the use of “quantitative” analysis of fisheries independent monitoring (FIM) data. A combination of these methods will probably be required in most situations as many FIM datasets exhibit disproportionate seasonal and geographic sampling effort. Results of preliminary analyses indicate that while empirical data will always be necessary to monitor trends in distribution and abundance, the qualitative data derived from scientific literature can provide reasonable estimations of these measures for estuarine species across broad spatial and temporal scales.

Figure 3. Continuum of approaches to evaluate the efficacy of SI derivation.



Recent Developments in Quantitative Analyses for HSI Modeling

Frequency Distribution Analysis to Determine Biologically Relevant Ranges

The following preliminary methodology can be used to determine biologically relevant environmental ranges for a species and/or life-history stage for HSI modeling. There is limited discussion of the use of cumulative frequencies to derive suitability index (SI) values in the *Proceedings of a Workshop on the Development and Evaluation of Habitat Suitability Criteria* (USFWS 1988). The first step is to create a dataset representing the group for which you want to determine ranges. The following example uses pinfish catch data from the state of Texas for which individual life-history stages are not split out. From this dataset plot a frequency of occurrence histogram for each environmental variable, in this case salinity (Figure 4). Then calculate a frequency score for each record by averaging the ranks of all records with the same salinity and scaling it from 0 to 1 (JMP Statistical Visualization Software, Version 2.0.5; SAS Institute Inc.). For a given salinity x (Table 2):

$$\text{Frequency Score of Record} = (\text{average Rank of all records with same salinity}) / (n+1).$$

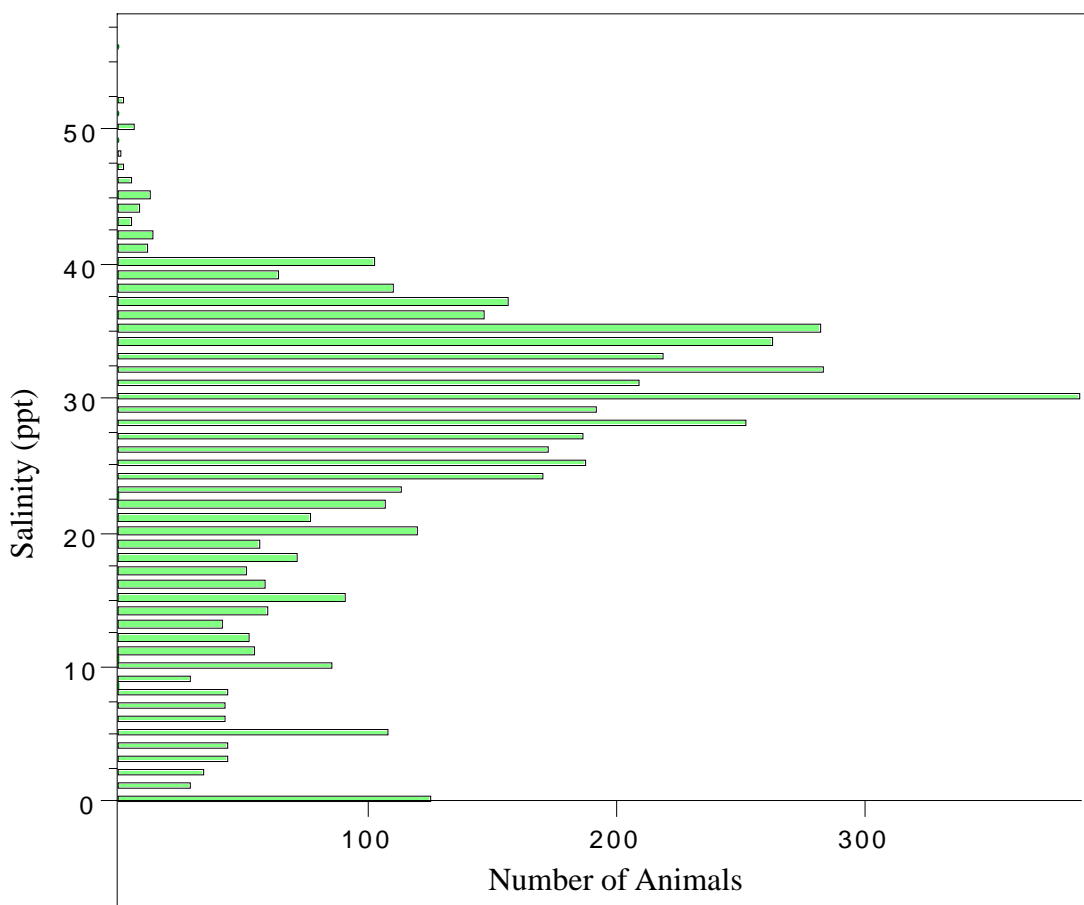


Figure 4. Frequency of occurrence histogram for pinfish caught in Texas calculated for salinity.

Table 2. An example of cumulative frequency score calculation based upon a salinity distribution.

Salinity	Rank	Cumulative Frequency Score
1	1	
1	2	
1	3	= average Rank / (n+1)
1	4	=average (1+2+3+4+5+6+7)/(500+1)
1	5	=4.5/501
1	6	0.01
1	7	
1	8	
.	.	
.	.	
18	253	
18	254	
18	255	
18	256	
18	257	0.51
18	258	
18	259	
18	260	
18	261	
.	.	
.	.	
35	485	
35	486	
35	487	
35	488	
35	489	
35	490	
35	491	
35	492	0.98
35	493	
35	494	
35	495	
35	496	
35	497	
35	498	
35	499	
35	500	

The next step is to plot salinity against the derived salinity frequency scores (Figure 5). This represent values with a similar frequency of occurrence. The key term to remember when looking at this plot is **cumulative**. Portions of this plot with the greatest slope represent greater frequency of occurrence, while a slope approaching zero represent a lower frequency of occurrence.

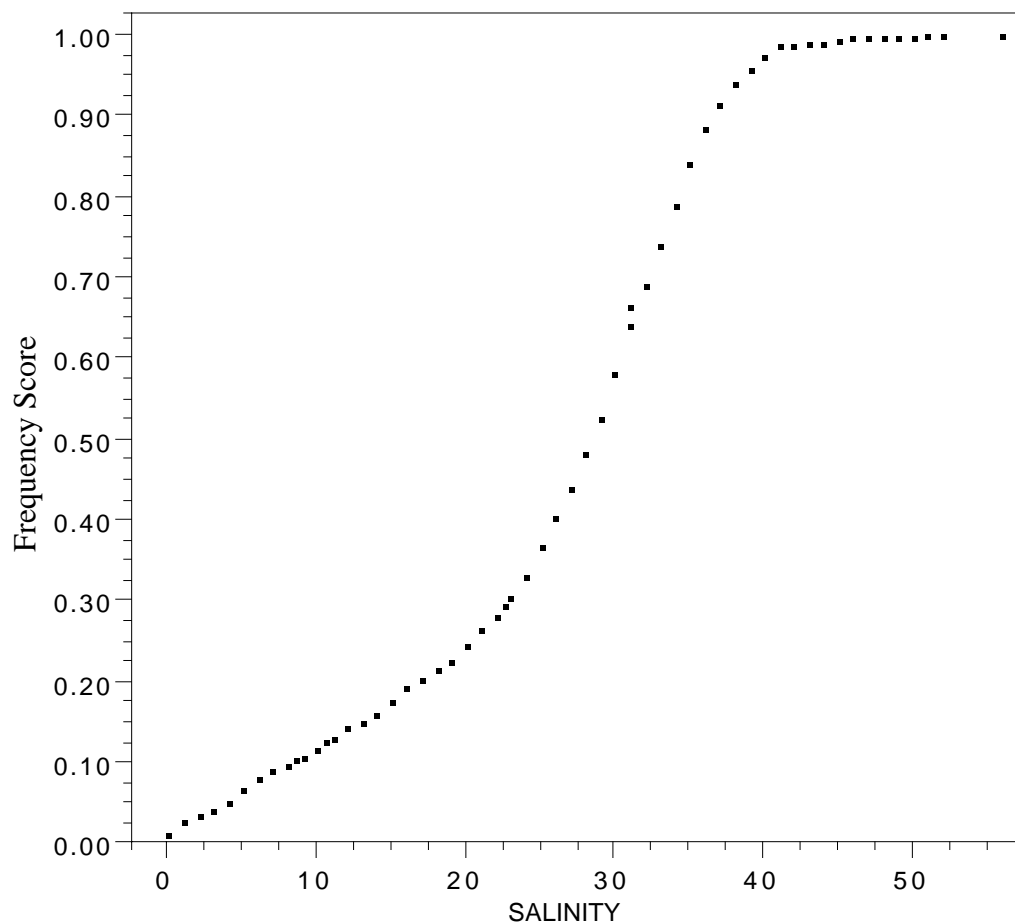


Figure 5. Plot of salinity against saved frequency scores for each record resulting in a cumulative frequency score curve.

You can now begin to draw straight lines through portions of the curve with a linear relationship (Figure 6). As mentioned previously, each range of points exhibiting a linear relationship have a similar frequency of occurrence. Points at which lines intersect are used to delimit each range. Each range must include at least three levels, or points, in order to fit a line. Obviously the more points the better the fit, but not all species or life-history stage ranges will necessarily be broad. Please note that some ranges may not become clear until the next step.

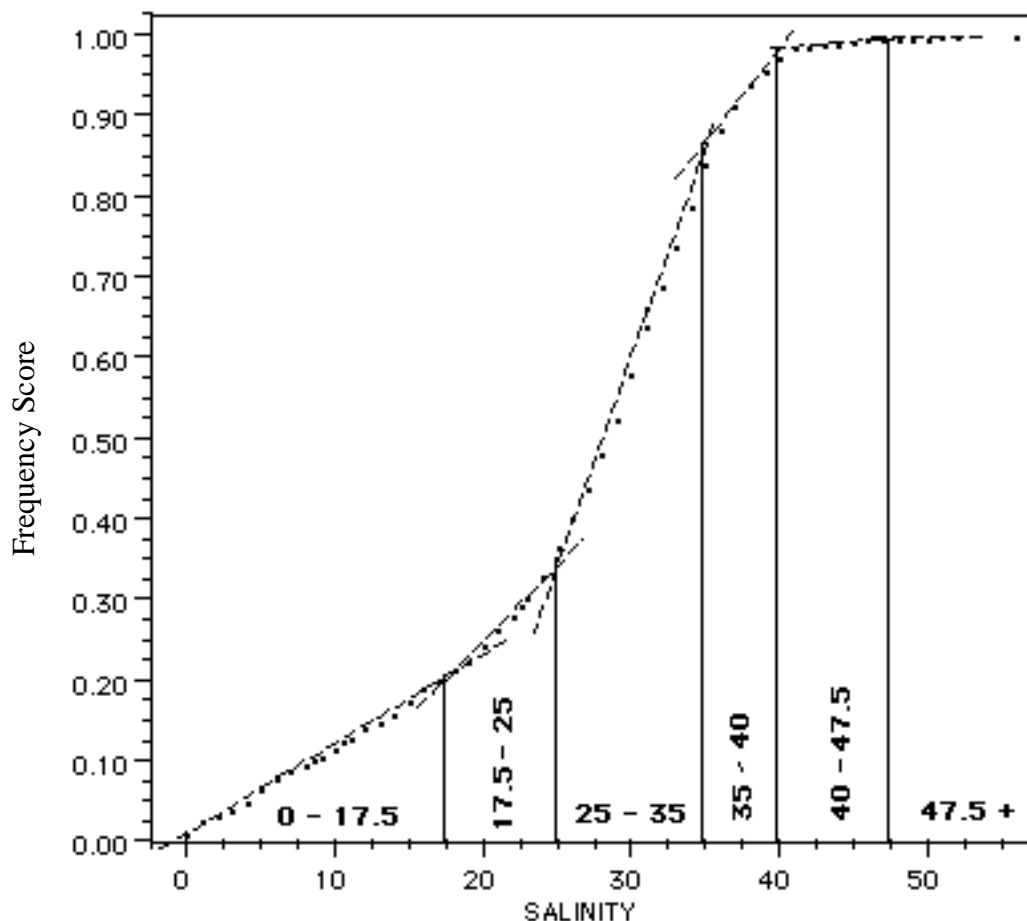
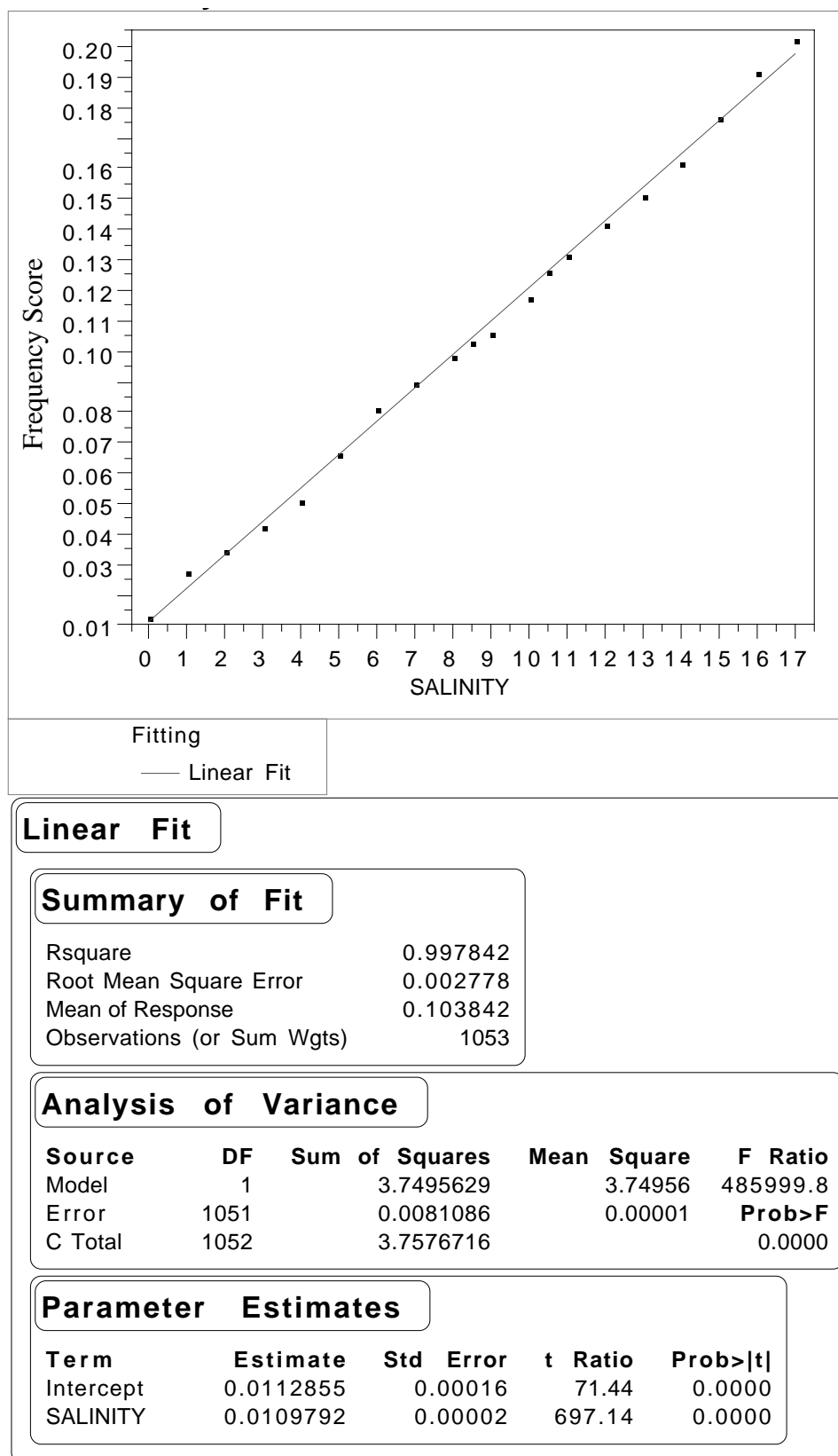


Figure 6. Linear relationships within the cumulative frequency score curve. Intersect points are used to delimit biologically relevant ranges.

Goodness of fit for each range can now be verified by regression analysis of salinity vs. salinity frequency score for a given range (Figure 7). Our preliminary work with this methodology suggests that a good measure of fit is an $R^2 \geq 0.90$ and $p \leq 0.05$. If you obtain an R^2 less than 0.90 you may find that points at either end of that particular range are not exactly linear when you zoom in on the plot. Experiment with removing outlying points at either end of the range and run the regression again. In this way you may modify your initial range estimates or create new ones.

Figure 7. Regression, fit and parameter estimates for 0 to 17.5 ppt salinity range by cumulative frequency score for pinfish in Texas.



When you have obtained a satisfactory fit, record the slope of the line. In the case of the salinity range 0 to 17.5 slope is equal to 0.0110. Repeat this step for each range recording the slope of each line (Table 3). Preliminary SI values can be estimated by dividing each slope by the maximum slope observed ($SI_{0-17.5} = 0.0110/0.0483 = 0.23$). These ranges can also be used to group environmental data into relevant biological ranges for additional analysis to obtain SI values.

Table 3. Slope and estimated suitability index (SI) values for each salinity range.

Salinity	Slope	SI Value
0- 17.5	0.0110	0.23
17.5- 25	0.0224	0.46
25- 35	0.0483	1.00
35- 40	0.0275	0.57
41- 47.5	0.0019	0.04
47.5+	0.0009	0.02

Empirical Predictive Models

SEA Division has been exploring methodologies to enable quantitative derivation of suitability index values (SI's) for HSI modeling. Our intent is to develop "seascape" views of habitat suitability across geographies which can be supported by a measure of statistical probability. Multiple regression techniques were chosen as most appropriate because they inherently account for biotic and abiotic interactions which have not traditionally been incorporated into HSI models. In past SEA efforts, some interactions were implied (i.e., salinity values as a surrogate measure of potential oyster drill densities and subsequent oyster mortality) in our SI values; however, not all interactions are as well documented and, more importantly, as simplistic. Multiple regression techniques take into account these interactions among model variables (salinity, temperature, D.O., etc.). Moreover, the use of robust fisheries independent data are presumed to be representative of the effects of all other possible interactions which may not be included in the analysis (i.e., predator-prey interactions, variable recruitment success, etc.).

In an attempt to assess the success and reliability of SEA Division's "qualitatively" derived (secondary data source) HSI models in Pensacola Bay, FL (Christensen et al. 1997), an empirical model was developed for eastern oyster (*Crassostrea virginica*). Our intent was threefold: 1) Compare spatial distribution pattern trends of both model approaches to ensure that "qualitative" and "quantitative" model designs were responding similarly to the composite of habitat variables; 2) evaluate the qualitative models predictive performance relative to a quantitative model design, and; 3) explore the concept of transferability across a range of geographies.

To address transferability, an empirical model was developed using Texas Parks & Wildlife Department (TPWD) fisheries independent monitoring data collected from 1987-94. Subsequent to the development of an acceptable model using these data, the resulting prediction formula was applied to Pensacola Bay environmental data and mapped in ARC-VIEW's spatial analyst module. A total of 700 observations were averaged into mean monthly abundance values, as were associated environmental information (salinity, temperature, D.O., and water depth). Data were treated in this manner to enable the calculation of salinity variability (variance) in the sampled space through time, which we believed to be a key factor determining the distribution and abundance of eastern oysters. Several models were then developed using both multiple linear and polynomial regressions, as well as stepwise linear and piecewise linear regression techniques. Final model selection was chosen based on the whole model fit significance, coupled with the significance of each individual component modeled in the regression (Figure 8). Variables which provided no significant contribution to the model were dropped entirely, and the multivariate model rerun.

To enable a comparison of model approaches (quantitative/qualitative), resulting HSI calculations were grouped into 5 categories as defined by quantiles. Data were parsed into 0-20, 20-40, 40-60, 60-80, and 80-100th percentile ranges. These ranges were then reclassified as 1, 2, 3, 4, and 5, respectively. Because our empirical model incorporated salinity variability, as measured by salinity variance (ρ^2) through an entire year, qualitative model results were combined across all four seasons

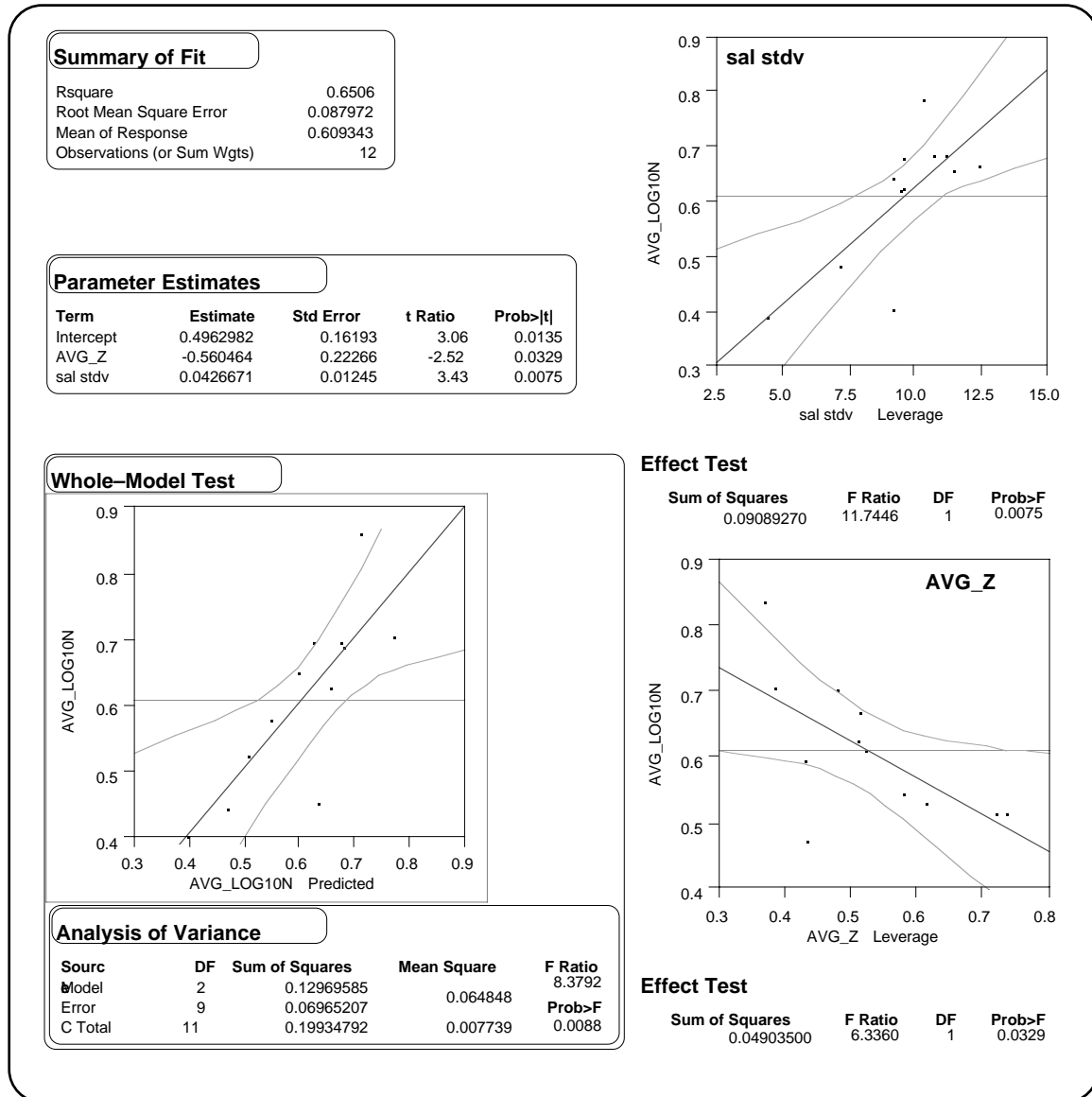


Figure 8. Multiple linear regression model developed for (log+1) transformed eastern oyster abundance using TPWD data.

modeled (see Christensen et al., 1997) to provide an annual view of oyster habitat suitability (Figure 8a).

Figures 9a and 9b represent the qualitative and empirical model results, respectively, while figure 9c is the calculated difference between the two. Negative values indicate an “overestimation” of habitat suitability by the qualitative model relative to that of the regression prediction, and positive numbers indicate the transpose. Observed oyster locations (Little and Quick, 1976) are plotted over the model results to provide an evaluation of model performance. The qualitative approach provided a more conservative estimate of habitat suitability in upper suitability classes. However, 100% of the observed oyster locations were contained in the highest quantile. The regression model appeared to perform extremely well, particularly in light of the transferability issue. Approximately

50% of the observed oysters fell in the 80-100% quantile, while the remainder was contained within the next lowest class. No oysters fell in the lowest 3 quantiles.

The empirical model exhibited higher sensitivity to water depth than did our previous models, resulting in a one HSI class shift down traveling from northeast to southwest. However, distribution patterns and the progression of HSI classes along each vector were the same. The empirical model also tended to overestimate the value of habitat in the lower portions of the bay. The model does not recognize salinity *per se*, but rather salinity variability. We also have developed a model which incorporates both approaches, and provides salinity threshold boundaries, as defined by our qualitative methods, in which the model is run. The resulting model indicates a significant decrease in suitability where annual average salinity is in excess of 20 ppt, or less than 10 ppt, while the remainder of the bay is predicted by the regression.

Ordination Techniques for Temporal Framework Selection

We suggest that modeling during two time periods (warm and cool water periods) may be sufficient, depending on your objectives. We ran principal components analysis on the TPWD data to investigate and support our hypothesis. We used all TPWD observations from their comprehensive bag seine and otter trawl surveys. Catch per unit effort was calculated for each observation (N=99, 051) and subsequently standardized. From this, we assembled data matrix consisting of average monthly CPUE for all species captured (N=67)(Table 4).

Rotated principal component axes indicated quite clearly that 2 components explain approximately 83% of the variance in the matrix. A third component, if included, explains an additional 5.4%. The first and strongest component consists of warm water months, while the second (and third) consist of cool water months, with an overlap of components during the month of May. These findings agree with work in Galveston Bay, TX (Christensen 1996). Christensen identified, using measures of community diversity (i.e., H', E, S) coupled with PCA, a summer-fall and winter-spring assemblage, dominated by hardhead catfish (*Arius felis*) and Gulf menhaden (*Brevoortia patronus*), respectively.

Figure 11 shows monthly positions along the first and second components. It is clear that a warm and cool water "assemblage" exists. A third component (only one to pick up the month of December) may or may not need be included based on a low eigenvalue and percent variance explained. It would be logical to include the month of December with component #2, as it overlaps with the remaining cool water months.

Habitat Suitability Index Modeling Eastern oyster: Pensacola Bay, FL.

HSI Reclassified into Quantiles (20%)

■ oyster point

■ reef

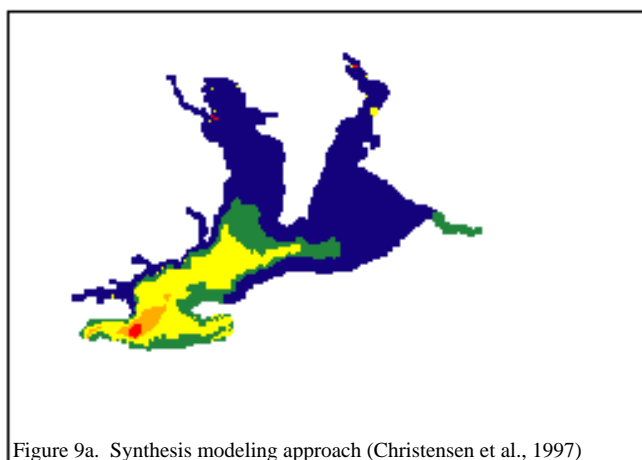
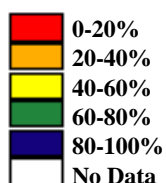


Figure 9a. Synthesis modeling approach (Christensen et al., 1997)

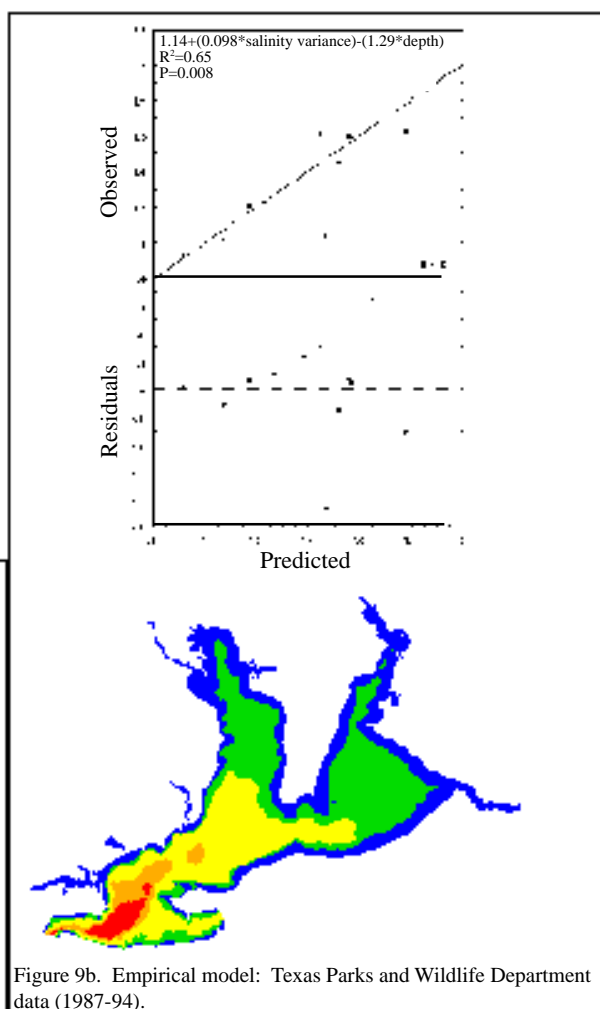


Figure 9b. Empirical model: Texas Parks and Wildlife Department data (1987-94).

Figure 9c. Map calculation showing difference in predicted quantile ranges.

Resulting grid represents the difference between the composite predictive grid and “quantitative” grid model outputs. The qualitative grid was developed using SEA division’s secondary search approach, whereas the quantitative grid was developed using multivariate statistical techniques. A prediction equation was developed using fisheries independent data from Texas Parks & Wildlife Department data (TPWD 1987-94). Both input grids were treated identically, and were parsed into 5 quantiles which were categorized as HSI classes 1 through 5 (0-20%=1, ..., 80-100%=5).

■ oyster point

■ reef

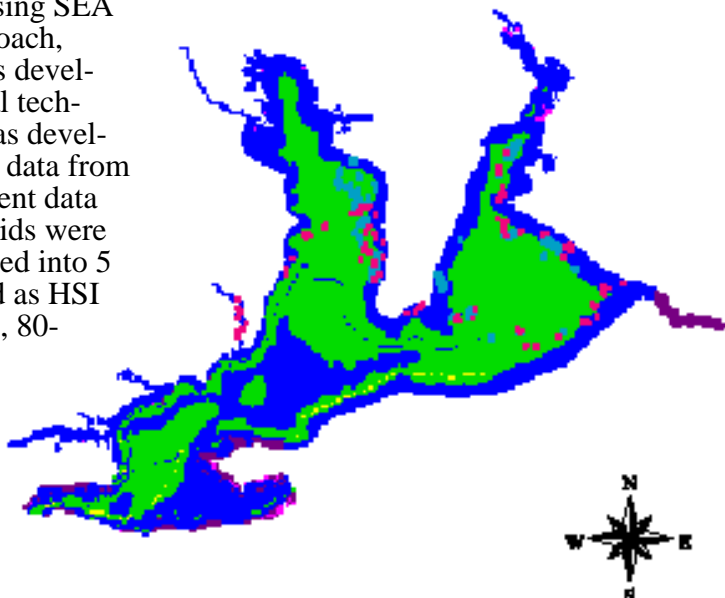
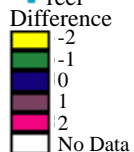


Table 4. Standardized species by month catch per unit effort matrix.

Species	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Atlantic bumper	0.77	1.02	0.98	1.31	1.02	1.28	1.52	1.78	1.78	1.96	1.22	1.37
Atlantic croaker	1.61	1.84	2.15	2.31	2.45	2.07	1.99	1.63	1.49	1.29	1.48	1.44
Atlantic cutlassfish	0.69	1.05	0.95	0.99	1.11	1.20	1.18	1.13	0.79	0.77	0.86	0.97
Atlantic spadefish	0.79	0.69	0.82	0.69	0.69	0.79	1.75	1.08	1.18	1.06	1.18	0.98
Atlantic stingray	0.83	0.81	0.87	0.84	0.85	0.80	0.85	0.93	0.90	0.85	0.86	0.78
Atlantic threadfin	1.61	0.69	0.00	0.61	1.15	1.31	1.42	1.36	1.25	0.93	0.85	0.00
banded drum	0.83	0.77	0.94	1.34	1.03	1.12	0.79	0.90	0.69	1.10	0.86	1.14
bay anchovy	1.29	1.45	1.43	1.41	1.50	1.35	1.40	1.46	1.51	1.55	1.29	1.47
bay whiff	1.00	1.07	0.88	0.93	1.00	0.95	0.99	0.98	0.89	0.91	0.99	0.98
big claw hermit crab	0.93	0.89	1.07	0.94	1.00	1.08	1.15	0.93	1.08	0.94	0.99	0.99
bighead searobin	1.08	1.07	1.08	0.98	0.90	0.93	0.79	0.63	0.65	0.82	0.86	0.97
balck drum	1.03	1.06	0.89	0.98	0.99	0.91	0.93	0.81	0.64	0.78	0.98	0.76
blachcheek tonguefish	0.23	0.91	1.01	1.11	1.02	1.02	0.93	0.88	0.81	0.97	0.81	0.42
blue crab	1.16	1.41	1.65	1.60	1.52	1.34	1.25	1.15	1.12	1.17	1.15	1.17
brief squid	1.63	1.86	2.03	2.22	1.81	1.80	1.76	1.64	1.54	2.03	2.12	2.15
brown shrimp	1.22	1.47	2.00	2.65	2.96	2.53	2.00	1.77	1.85	1.96	1.73	1.34
brokenback shrimp	1.49	1.41	1.70	1.86	1.43	1.08	1.24	0.00	1.24	1.07	1.52	1.38
Florida pompano	0.00	0.00	0.00	0.17	0.97	0.99	0.70	0.75	0.37	0.37	0.54	0.41
fringed flounder	0.85	0.98	1.02	1.03	0.87	0.96	0.95	0.89	0.91	0.89	1.03	0.85
gaftopsail catfish	0.00	1.32	1.27	0.91	0.69	0.69	1.67	1.43	1.06	1.01	0.69	0.69
grass shrimp	1.62	1.94	1.75	1.77	1.74	1.63	1.81	2.14	1.94	1.64	1.85	2.18
Gulf butterflyfish	1.19	1.36	1.39	1.54	1.49	1.17	1.44	1.07	0.89	0.98	0.87	1.23
Gulf flounder	0.69	0.69	1.10	0.93	0.85	0.82	0.90	0.74	1.03	0.69	0.76	0.69
Gulf killifish	1.25	1.37	1.27	1.28	1.19	1.28	1.51	1.14	0.99	1.10	1.26	1.39
Gulf kingfish	0.58	0.37	0.00	0.51	0.00	0.28	0.00	0.46	0.35	0.05	0.34	0.97
Gulf menhaden	1.58	1.72	1.82	2.03	2.02	1.60	1.45	1.40	1.38	1.32	1.35	1.59
Gulf toadfish	0.86	1.15	0.81	1.07	1.08	1.15	1.22	1.41	1.69	1.26	1.22	1.31
Gulf harvestfish	0.69	0.76	0.86	0.89	0.77	1.07	1.29	0.95	0.90	1.09	1.20	0.90
hardhead catfish	1.05	1.26	1.32	1.27	1.29	1.26	1.44	1.45	1.44	1.35	1.32	0.92
inland silverside	1.29	1.35	1.48	1.20	1.48	1.27	1.45	1.36	1.49	1.40	1.65	1.26
least puffer	0.92	0.86	0.90	0.91	1.23	1.16	0.90	0.93	1.02	1.26	1.24	0.96
leatherjacket	0.00	0.00	0.00	0.69	0.69	0.86	0.71	0.89	0.93	1.02	0.75	1.87
lesser blue crab	1.01	1.15	1.67	1.54	1.76	1.68	1.48	1.17	1.30	1.30	1.43	1.13
lightning whelk	0.69	0.91	0.76	0.69	0.88	0.74	0.86	1.10	0.69	0.79	0.69	1.39
longclaw hermit crab	0.87	0.83	0.87	0.79	0.83	0.69	0.91	0.69	0.69	0.77	0.88	0.69
longnose killifish	1.47	1.60	1.65	1.82	2.02	1.68	2.02	1.88	1.74	1.84	1.74	1.68
lookdown	0.69	0.69	0.00	0.69	1.34	0.99	1.11	1.00	0.81	0.81	0.87	0.79
mantis shrimp	1.45	1.16	1.12	1.05	1.11	0.86	0.86	0.96	1.02	1.00	1.35	1.19
naked goby	0.81	0.66	0.51	0.78	0.51	1.03	1.07	1.29	1.18	1.00	1.00	0.83
pigfish	1.07	1.49	1.23	1.14	1.24	1.52	1.77	1.64	1.62	1.56	1.38	0.95
pinfish	2.05	2.26	2.18	2.40	2.49	2.28	2.21	2.06	1.90	1.96	2.23	2.15
pink shrimp	1.10	1.24	1.45	1.63	1.64	0.93	0.87	1.05	1.18	0.99	1.43	1.28
purple crab	1.10	0.92	0.97	0.91	0.90	0.87	0.96	0.86	0.95	1.07	1.31	1.25
red drum	0.94	1.12	1.12	0.73	0.83	0.72	0.81	0.73	0.74	0.99	1.25	1.19
sand seatrout	1.06	1.16	1.30	1.35	1.41	1.36	1.46	1.22	1.24	1.07	1.10	1.24
seabob	2.20	0.93	1.07	1.52	1.57	1.78	2.16	1.43	1.92	1.04	2.36	1.77
sheepshead minnow	1.81	1.91	1.92	1.72	1.81	1.98	2.41	2.00	1.69	1.80	1.98	2.42
sheepshead	0.79	0.85	0.72	0.89	1.01	0.80	0.89	0.89	0.92	0.86	0.93	0.80
silver jenny	0.00	0.00	0.00	0.69	1.53	2.03	1.93	1.60	0.95	1.27	1.21	0.67
silver perch	1.41	1.37	1.24	1.27	1.31	1.40	1.54	1.54	1.48	1.49	1.36	1.25
silver seatrout	1.05	1.23	1.69	2.53	1.65	1.89	1.52	1.75	1.53	0.84	1.72	0.79
smooth puffer	0.00	0.69	1.10	0.69	0.69	1.13	0.69	0.69	0.79	0.69	0.00	0.69
snook	0.00	0.00	0.00	0.69	0.00	0.00	0.00	0.00	0.00	0.69	0.69	0.00
southern flounder	0.74	1.10	0.89	0.80	0.69	0.61	0.62	0.58	0.69	0.67	0.60	0.73
southern hake	0.83	0.80	0.88	1.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
southern kingfish	0.98	0.85	0.81	0.96	0.81	0.97	0.98	0.87	1.01	0.83	0.76	0.79
spot	1.99	2.04	2.36	2.30	2.25	2.07	2.11	1.90	1.68	1.59	1.84	1.80
spotfin mojarra	0.00	1.39	0.69	2.23	1.70	1.83	1.60	2.01	1.70	1.78	1.51	1.37
spotted seatrout	0.96	1.03	0.69	0.79	0.69	0.97	0.85	1.06	1.18	1.18	0.84	0.77
star drum	1.23	1.01	1.29	1.18	1.10	1.71	1.79	1.17	1.73	1.68	1.84	1.64
striped burrfish	1.42	1.23	1.40	1.20	0.94	0.93	0.87	1.11	1.05	0.99	1.35	1.21
striped hermit crab	0.91	0.99	1.34	1.22	1.41	1.26	1.36	1.30	1.24	1.18	1.19	1.02
striped mullet	1.25	1.36	1.43	1.30	1.41	1.32	1.10	1.12	1.11	0.95	1.05	1.29
threadfin shad	1.04	1.03	0.98	0.83	0.79	0.92	0.92	1.40	1.31	1.08	1.11	1.26
tidewater silverside	2.06	1.78	1.79	1.87	1.60	2.00	1.89	1.78	1.79	1.90	1.97	2.03
white mullet	2.02	1.89	2.10	1.74	2.11	2.55	2.19	1.89	1.53	1.19	1.14	1.21
white shrimp	1.67	1.35	1.39	1.46	1.18	1.89	2.02	2.10	2.08	2.17	1.98	1.67

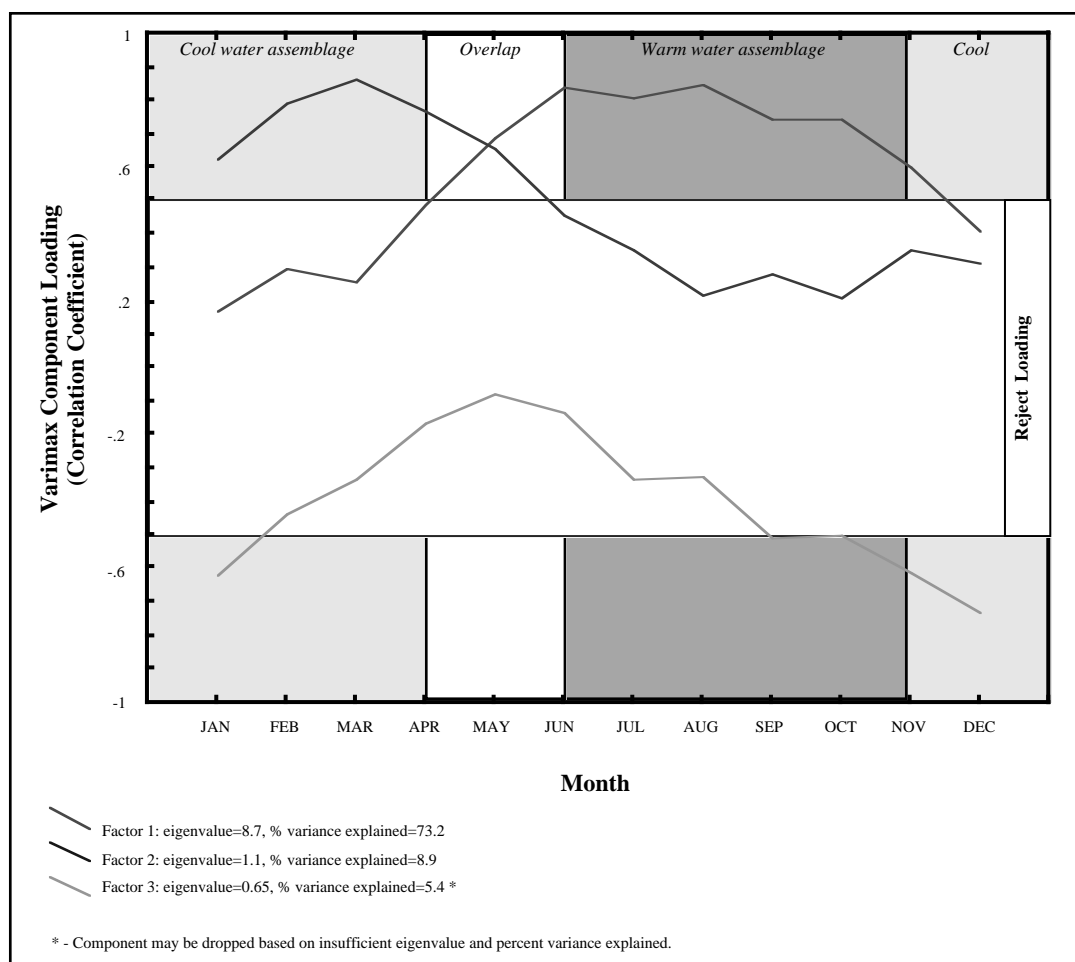


Figure 10. Varimax rotated principal component loadings for each month.

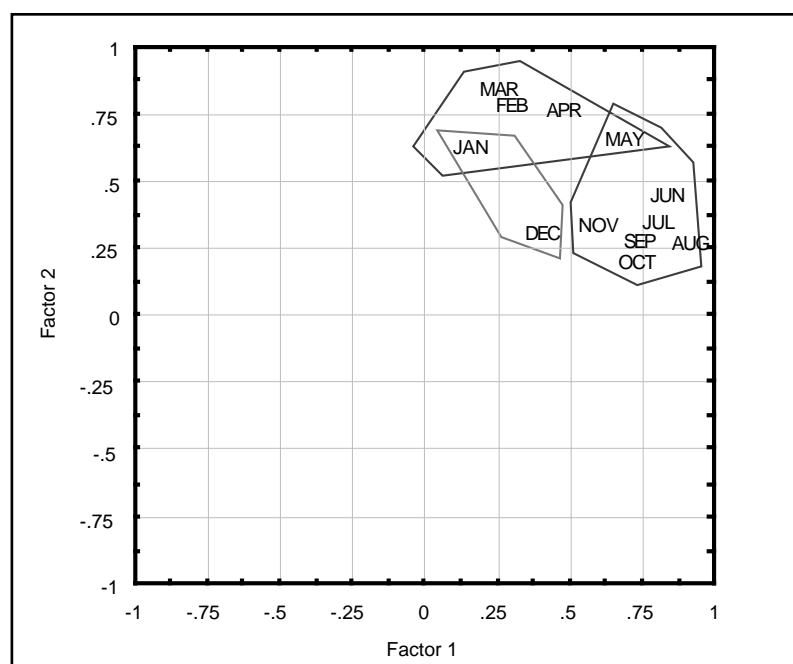


Figure 11. Biplot of month locations along the first and second principal component axes.

Quantitative Habitat Affinity Indices (HAI)

We have analyzed time-series data sets that contained species catch by their habitat variables to measure the repeatability of a species' response to environmental parameters (Monaco et al. in press). We quantified species habitat affinities based on the relative concentration of a species in a specific habitat (e.g., depth zone) when compared to the relative availability of that habitat throughout the study area. To quantify species habitat affinities, we developed a habitat affinity index (HAI) based on a modification of the Strauss (1979) electivity index:

$$\text{HAI} = (p - r) / r, \text{ if } p \leq r$$

or

$$\text{HAI} = (p - r) / (1 - r), \text{ if } p \geq r$$

where p is the proportion of species collected in a specific habitat and r is the proportion of area that habitat comprises in the study area.

The HAI has a center point of zero; therefore, the index is scaled so that an HAI of -1 corresponds to non-collection or complete avoidance of an area (Table 5). An HAI of 0 indicates that fish displayed no habitat affinity, and an HAI of +1 indicates an apparent exclusive affinity for a specific habitat zone or area. Negative values (other than -1) are used to define avoidance, and are not equivalent to complete absence; a negative HAI value in the electivity context reflects a lesser concentration of a species in a particular habitat. These HAI values can be scaled, from 0 to 1 for example, for use SI values in HSI modeling.

Table 5. Species Habitat Affinity Index values for environmental and geographic variables in the mid-Atlantic region. Shaded values indicate a statistically significant affinity (+) or avoidance (-) (Monaco et al. in review).

SPECIES Life stage		SALINITY ZONES (ppt)					SUBSTRATE (% SILT/CLAY)		
		0 - 0.5	0.5 - <5	5 - < 15	15 - < 25	> 25	0 < 20	20 - ≤ 80	> 80
SPOT	AVG HPI	-0.939	0.012	0.164	0.380	-0.816	-0.577	-0.057	0.304
Juvenile	STD ERROR	0.047	0.006	0.091	0.103	0.059	0.144	0.103	0.191
WEAKFISH	AVG HPI	-1.000	-1.000	-0.792	0.646	-0.542	-0.618	0.220	-0.242
Adult	STD ERROR	0.000	0.000	0.202	0.202	0.325	0.180	0.371	0.377
HOGCHOKER	AVG HPI	-0.014	0.244	0.119	-0.668	-0.898	-0.719	-0.546	0.649
Juvenile	STD ERROR	0.065	0.280	0.406	0.083	0.102	0.133	0.211	0.127

Concluding Comments

This “springboard” for discussion paper was developed in support of the Florida Estuarine Living Marine Resources project. These suggested analyses will be refined using FMRI’s qualitative fisheries independent monitoring. The joint NOAA and FMRI study is underway in Tampa Bay and Charlotte Harbor.

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